WEST Search History

DATE: Wednesday, July 30, 2003

Set Name side by side	Query	Hit Count	Set Name result set
DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR			
L8	L7 and receptor adj4 domain	95	L8
L7	L6 and selection adj3 marker	424	L7
L6	L3 and envelope adj2 protein	1625	L6
L5	L3 and (random adj4 display adj4 library adj4 retrovirus)	0	L5
L4	L3 and random adj4 display adj4 library adj4 retrovirus	0	L4
L3	L2 and mammalian adj4 cell	17095	L3
L2	retrov$6	30142	L2
L1	random adj6 library adj5 retrovirus	8	L1

END OF SEARCH HISTORY

FILE 'CA, BIOSIS, MEDLINE' ENTERED AT 17:06:11 ON 30 JUL 2003

L1 0 S TARGE?(5W)RETROV?(5W)VECTOR(5W)MAMMAL?

L2 720889 S RETRO?

L3 6 S L2 AND RANDOM(5W)LIB?(5W)RETRO?

TI B epitopes and selection pressures in feline immunodeficiency **virus** envelope glycoproteins.

AU Pancino G; Chappey C; Saurin W; Sonigo P

SO JOURNAL OF VIROLOGY, (1993 Feb) 67 (2) 664-72.
Journal code: 0113724. ISSN: 0022-538X.

PY 1993

AB In order to map linear B epitopes in feline immunodeficiency **virus** (FIV) envelope glycoproteins (Env), a **random library** of FIV Env polypeptides fused to beta-galactosidase and expressed in Escherichia coli was screened by using sera from experimentally FIV-infected cats. We mapped five antibody-binding domains in the surface envelope glycoprotein (SU1 to SU5) and four in the transmembrane envelope glycoprotein (TM1 to TM4). Immunological analysis with 48 serum samples from naturally or experimentally infected cats of diverse origins revealed a broad group reactivity for epitopes SU2, TM2, and TM3, whereas SU3 appeared as strictly type specific. To study selection pressures acting on the identified immunogenic domains, we analyzed structural constraints and distribution of synonymous and nonsynonymous mutations (amino acids unchanged or changed). Two linear B epitopes (SU3 and TM4) appeared to be submitted to positive selection for change, a pattern of evolution predicting their possible involvement in antiviral protection. These experiments provide a pertinent choice of oligopeptides for further analysis of the protective response against FIV envelope glycoproteins, as a model to understand the role of antibody escape in lentiviral persistence and to design feline AIDS vaccines.

2002

AB Tissue-specific gene delivery is an important aspect of many gene therapy applications. The expts. reported here constitute the first successful demonstration that cell-specific entry can be obtained by screening a random library of retroviral envelope proteins produced from a mammalian cell system. The library consisted of 106 different subgroup A feline leukemia **virus** envelope protein variants with 10 randomly substituted amino acids in the receptor-detg. region. Selecting the library for fully functional envelope proteins able to mediate stable gene transfer resulted in the identification of a single envelope protein variant (EF). Subsequent examn. of the host range of EF revealed that it was highly specific for D17 canine osteosarcoma cells. This was in contrast to the host ranges of the parental subgroup A and closely related sub-group C envelope proteins. Interference assays on D17 cells further indicated that receptor usage by EF was also altered compared with the A and C envelope proteins. The EF envelope protein thus isolated should be useful for studying gene therapy treatments of osteosarcoma in a large-animal model.

L3 ANSWER 1 OF 6 CA COPYRIGHT 2003 ACS on STN
TI Altering **retroviral** tropism using a random-display envelope library
AU Bupp, Keith; Roth, Monica J.
SO Molecular Therapy (2002), 5(3), 329-335
CODEN: MTOHCK; ISSN: 1525-0016
PY 2002
AB Tissue-specific gene delivery is an important aspect of many gene therapy applications. The expts. reported here constitute the first successful demonstration that cell-specific entry can be obtained by screening a **random library** of **retroviral** envelope proteins produced from a mammalian cell system. The library consisted of 106 different subgroup A feline leukemia virus envelope protein variants with 10 randomly substituted amino acids in the receptor-detg. region. Selecting the library for fully functional envelope proteins able to mediate stable gene transfer resulted in the identification of a single envelope protein variant (EF). Subsequent examn. of the host range of EF revealed that it was highly specific for D17 canine osteosarcoma cells. This was in contrast to the host ranges of the parental subgroup A and closely related sub-group C envelope proteins. Interference assays on D17 cells further indicated that receptor usage by EF was also altered compared with the A and C envelope proteins. The EF envelope protein thus isolated should be useful for studying gene therapy treatments of osteosarcoma in a large-animal model.

L3 ANSWER 2 OF 6 CA COPYRIGHT 2003 ACS on STN
TI Isolation of genetic suppressor elements (GSEs) from **random** fragment cDNA **libraries** in **retroviral** vectors
AU Gudkov, Andrei V.; Roninson, Igor B.
SO Methods in Molecular Biology (Totowa, New Jersey) (1997), 69(cDNA Library Protocols), 221-240
CODEN: MMBIED; ISSN: 1064-3745
PY 1997
AB The identification and functional anal. of recessive genes in mammalian cells have been boosted by the ability to select genetic suppressor elements (GSEs) that induce the desired phenotype by suppression of specific genes. GSEs are short (<500 bp) cDNA fragments that produce a phenotype when expressed in cells, this phenotype is usually opposite to that of the full-length cDNA from which they are derived. GSEs inhibiting recessive genes behave as dominant selectable markers in gene-transfer protocols and can therefore serve as tools for studying recessive mechanisms. There are two types of GSE: antisense-oriented GSEs encoding efficient inhibitory antisense RNA mols. and sense-oriented GSEs encoding functional protein domains that interfere with the protein function in a dominant fashion. GSEs are isolated by prepg. an expression library contg. randomly fragmented DNA of the gene or genes targeted for suppression, introducing this library into the appropriate recipient cells, selecting cells with the desired phenotype, recovering the inserts from the expression vectors contained in the selected cells, and testing the recovered sequences for functional activity. A method is described to do so.

L3 ANSWER 3 OF 6 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI **Retrovirally** delivered random cyclic peptide libraries yield inhibitors of interleukin-4 signaling in human B cells.
AU Kinsella, Todd M.; Ohashi, Cara T.; Harder, Amy Grace; Yam, George C.; Li, Weiqun; Peelle, Beau; Pali, Erlina S.; Bennett, Mark K.; Molineaux, Susan M.; Anderson, D. A.; Masuda, Esteban S.; Payan, Donald G. (1)
SO Journal of Biological Chemistry, (October 4, 2002) Vol. 277, No. 40, pp. 37512-37518. http://www.jbc.org/. print.
ISSN: 0021-9258.
PY 2002
AB Inteins are polypeptide sequences found in a small set of primarily

bacterial proteins that promote the splicing of flanking pre-protein sequences to generate mature protein products. Inteins can be engineered in a "split and inverted" configuration such that the protein splicing product is a cyclic polypeptide consisting of the sequence linking two intein subdomains. We have engineered a split intein into a **retroviral** expression system to enable the intracellular delivery of a library of random cyclic peptides in human cells. Cyclization of peptides could be detected in cell lysates using mass spectrometry. A functional genetic screen to identify 5-amino acid-long cyclic peptides that block interleukin-4 mediated IgE class switching in B cells yielded 13 peptides that selectively inhibited germ line epsilon transcription. These results demonstrate the generation of cyclic peptide libraries in human cells and the power of functional screening to rapidly identify biologically active peptides.

L3 ANSWER 4 OF 6 BIOSIS COPYRIGHT 2003 BIOLOGICAL ABSTRACTS INC. on STN
TI Isolation of genetic suppressor elements (GSEs) from **random** fragment cDNA **libraries** in **retroviral** vectors.
AU Gudkov, Andrei V.; Roninson, Igor B.
SO Cowell, I. G. [Editor]; Austin, C. A. [Editor]. Methods in Molecular Biology, Vol. 69, pp. 221-240. Methods in Molecular Biology; cDNA library protocols.
Publisher: Humana Press Inc. Suite 808, 999 Riverview Drive, Totowa, New Jersey 07512, USA.
ISSN: 0097-0816. ISBN: 0-89603-383-X.

L3 ANSWER 5 OF 6 MEDLINE on STN
TI Altering **retroviral** tropism using a random-display envelope library.
AU Bupp Keith; Roth Monica J
SO MOLECULAR THERAPY, (2002 Mar) 5 (3) 329-35.
Journal code: 100890581. ISSN: 1525-0016.
PY 2002
AB Tissue-specific gene delivery is an important aspect of many gene therapy applications. The experiments reported here constitute the first successful demonstration that cell-specific entry can be obtained by screening a **random library** of **retroviral** envelope proteins produced from a mammalian cell system. The library consisted of 10(6) different subgroup A feline leukemia virus envelope protein variants with 10 randomly substituted amino acids in the receptor-determining region. Selecting the library for fully functional envelope proteins able to mediate stable gene transfer resulted in the identification of a single envelope protein variant (EF). Subsequent examination of the host range of EF revealed that it was highly specific for D17 canine osteosarcoma cells. This was in contrast to the host ranges of the parental subgroup A and closely related subgroup C envelope proteins. Interference assays on D17 cells further indicated that receptor usage by EF was also altered compared with the A and C envelope proteins. The EF envelope protein thus isolated should be useful for studying gene therapy treatments of osteosarcoma in a large-animal model.

L3 ANSWER 6 OF 6 MEDLINE on STN
TI Isolation of genetic suppressor elements (GSEs) from **random** fragment cDNA **libraries** in **retroviral** vectors.
AU Gudkov A V; Roninson I B
SO METHODS IN MOLECULAR BIOLOGY, (1997) 69 221-40.
Journal code: 9214969. ISSN: 1064-3745.
PY 1997

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(FILE 'HOME' ENTERED AT 17:05:53 ON 30 JUL 2003)